Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

Claim 1 (Currently amended):   A method for modeling cellular metabolism of an organism, comprising:

constructing on a computer a flux balance analysis model utilizing stoichiometric mass balances of metabolic and cellular composition information of the organism to identify stoichiometric boundaries for available flux distributions of a metabolic network;

applying logic constraints comprising a regulation matrix to the flux balance analysis model to produce an altered flux balance analysis model, wherein said logic constraints constrain one of said identified stoichiometric boundaries for one of said available flux distributions, wherein said altered flux balance analysis model has improved predictive capabilities of cellular metabolism of the organism over said flux balance analysis model and thereby provides a model of cellular metabolism of the organism; and

providing an output to a user of said available flux distribution having said constrained stoichiometric boundary.

Claim 2 (Previously presented):   The method of claim 1 wherein the logic constraints are capable of protecting against violation of a kinetic barrier.

Claim 3 (Previously presented):   The method of claim 1 wherein the logic constraints further include a set of connectivity restraints.

Claim 4 (Previously presented):   The method of claim 1 further comprising the step of applying mixed-integer linear programming to said altered flux balance analysis model having improved predictive capabilities to solve for a desired metabolic outcome.

Claim 5 (Original):   The method of claim 1 further comprising the step of solving for a desired metabolic outcome.

Claim 6 (Currently amended):   A method for modeling cellular metabolism of an organism that improves upon a flux balance analysis model, comprising:

constructing on a computer the flux balance analysis model utilizing stoichiometric mass balances of
      metabolic and cellular composition information of the organism to identify stoichiometric
      boundaries for available flux distributions of a metabolic network;

applying a plurality of logic constraints comprising a regulation matrix to the flux balance analysis
      model to produce an altered flux balance analysis model, wherein said plurality of logic
      constraints constrain one of said identified stoichiometric boundaries for one of said available
      flux distributions, wherein said altered flux balance analysis model has improved predictive
      capabilities of cellular metabolism of the organism over said flux balance analysis model and
      thereby provides a model of cellular metabolism of the organism; and

providing an output to a user of said available flux distribution having said constrained stoichiometric
      boundary.

Claim 7 (Previously presented):   The method of claim 6, further comprising selecting the set of logic constraints to protect against violation of a kinetic or regulatory barrier.

Claim 8 (Original):   The method of claim 6 wherein the logic constraints are defined by a relationship between changes in reaction fluxes and metabolic concentrations.

Claim 9 (Cancelled).

Claim 10 (Original):   The method of claim 6 wherein the logic constraints are represented by binary variables.

Claim 11 (Original):   The method of claim 10 wherein a first binary variable represents the presence of a reaction and a second binary variable represents the absence of a reaction.

Claim 12 (Original):   The method of claim 6 further comprising applying a computational procedure to identify a minimal set of metabolic reactions.

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Claim 13 (Original):   The method of claim 12 further comprising selecting a growth rate, and wherein the step of applying a computational procedure is applying a computational procedure to identify the minimal set of metabolic reactions capable of supporting the growth rate.

Claim 14 (Previously presented):   The method of claim 6 further comprising the step of applying mixed-integer linear programming to said altered flux balance analysis model having improved predictive capabilities to solve for a desired metabolic outcome.

Claim 15 (Previously presented):   The method of claim 6 further comprising the step of solving for a desired metabolic outcome.

Claim 16 (Previously presented):   The method of claim 15 further comprising engineering a change in an organism to produce the desired metabolic outcome.

Claims 17-18 (Cancelled).

Claim 19 (Currently amended):   A ~~computer readable medium having stored thereon a~~ system for modeling cellular metabolism of an organism, comprising:

a flux balance analysis model <u>contained on a computer readable medium</u> utilizing stoichiometric mass
  balances of metabolic and cellular composition information of the organism to identify
  stoichiometric boundaries for available flux distributions of a metabolic network;

a plurality of logic constraints comprising a regulation matrix applied to the flux balance analysis
  model, the logic constraints selected from the set consisting of qualitative kinetic information
  constraints, qualitative regulatory information constraints, and differential DNA microarray
  experimental data constraints; and

commands <u>for execution on a computer</u> for producing an altered flux balance analysis model wherein
  said plurality of logic constraints constrain one of said identified stoichiometric boundaries for
  one of said available flux distributions, wherein said altered flux balance analysis model has
  improved predictive capabilities of cellular metabolism of the organism over said flux balance
  analysis model and thereby provides a model of cellular metabolism of the organism.

Claim 20 (Previously presented):   The method of claim 1 wherein the logic constraints further include qualitative regulatory information constraints.

Claim 21 (Previously presented):   The method of claim 20 wherein the logic constraints protect against violation of a regulatory barrier.

Claim 22 (Previously presented):   The method of claim 1 wherein the logic constraints further include DNA microarray experimental data constraints.

Claim 23 (Currently amended):   A method for modeling cellular metabolism of an organism, comprising:

constructing on a computer a flux balance analysis model of a metabolic network of the organism;

applying constraints to the flux balance analysis model, wherein the constraints include qualitative
      kinetic information constraints, qualitative regulatory information constraints, differential DNA
      microarray experimental data constraints, or a combination thereof;

producing an altered flux balance analysis model wherein said constraints constrain a stoichiometric
      boundary for an available flux distribution, wherein said altered flux balance analysis model
      has improved predictive capabilities of cellular metabolism of the organism over said flux
      balance analysis model and thereby provides a model of cellular metabolism of the organism;
      and

providing an output to a user of said available flux distribution having said constrained stoichiometric
      boundary.

Claim 24 (Previously presented):   The method of claim 23 wherein the constraints include logic constraints to protect against violation of a regulatory barrier.

Claim 25 (Previously presented):   The method of claim 23 wherein the constraints further include connectivity restraints.

Claim 26 (Previously presented):   The method of claim 23 further comprising applying mixed-integer linear programming to said altered flux balance analysis model having improved predictive capabilities to solve for a desired metabolic outcome.

Claim 27 (Previously presented):   The method of claim 23 further comprising solving for a desired metabolic outcome.

Claims 28-29 (Cancelled).

Claim 30 (Currently amended):   A method for modeling cellular metabolism of an organism that improves upon a flux balance analysis model, comprising:

constructing on a computer the flux balance analysis model utilizing stoichiometric mass balances of metabolic and cellular composition information of the organism to identify stoichiometric boundaries for available flux distributions of a metabolic network;

applying a plurality of logic constraints comprising a regulation matrix to the flux balance analysis model to produce an altered flux balance analysis model, wherein said plurality of logic constraints constrain one of said identified stoichiometric boundaries for one of said available flux distributions, wherein said altered flux balance analysis model has improved predictive capabilities of cellular metabolism of the organism over said flux balance analysis model; applying mixed-integer linear programming to said altered flux balance analysis model having improved predictive capabilities to solve for a desired metabolic outcome of the altered flux balance analysis model, thereby modeling cellular metabolism of the organism; and

providing an output to a user of the application of mixed-integer linear programming to solve for a desired metabolic outcome.

Claim 31 (Previously presented):   The method of claim 30 further comprising the step of solving for the desired metabolic outcome.

Claim 32 (Previously presented):   The method of claim 31 further comprising engineering a change in the organism to produce the desired metabolic outcome.

Claim 33 (Currently amended): A method for modeling cellular metabolism of an organism, comprising:

constructing on a computer a flux balance analysis model using stoichiometric mass balances of metabolic and cellular composition information of the organism to identify stoichiometric boundaries for available flux distributions of a metabolic network;

determining logic constraints comprising a regulation matrix to apply to the flux balance analysis model, the logic constraints based on qualitative relationships between changes in reaction fluxes and changes in metabolite concentrations;

applying the logic constraints to the flux balance analysis model to produce an altered flux balance analysis model, wherein said logic constraints constrain one of said identified stoichiometric boundaries for one of said available flux distributions, wherein said altered flux balance analysis model has improved predictive capabilities of cellular metabolism of the organism over said flux balance analysis model and thereby provides a model of cellular metabolism of the organism; and

providing an output to a user of said available flux distribution having said constrained stoichiometric boundary.

Claim 34 (Currently amended): The ~~computer readable medium~~ system of claim 19, wherein said constraints comprise qualitative kinetic information constraints.

Claim 35 (Currently amended): The ~~computer readable medium~~ system of claim 19, wherein said constraints comprise qualitative regulatory information constraints.

Claim 36 (Currently amended): The ~~computer readable medium~~ system of claim 19, wherein said constraints comprise differential DNA microarray experimental data constraints.

Claim 37 (Previously presented): The method of claim 23, wherein said constraints include qualitative kinetic information constraints.

Claim 38 (Previously presented): The method of claim 23, wherein said constraints include qualitative regulatory information constraints.

Claim 39 (Previously presented): The method of claim 23, wherein said constraints include differential DNA microarray experimental data constraints.